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RAW SEQUENCE LISTING

DATE: 09/02/2004

PATENT APPLICATION: US/10/813,588

TIME: 07:43:28

Input Set : N:\Crf3\RULE60\10813588.raw.txt

Output Set: N:\CRF4\09022004\J813588.raw

1 <110> APPLICANT: Donoho, Gregory
 2 Turner, C. Alexander Jr.
 3 Nehls, Michael
 4 Friedrich, Glenn
 5 Zambrowicz, Brian
 6 Sands, Arthur T.
 7 <120> TITLE OF INVENTION: Novel Human Proteins and Polynucleotides
 8 Encoding the Same
 9 <130> FILE REFERENCE: LEX-0071-USA
 10 <140> CURRENT APPLICATION NUMBER: US/10/813,588
 C--> 11 <141> CURRENT FILING DATE: 2004-03-30
 12 <150> PRIOR APPLICATION NUMBER: US/09/691,344
 13 <151> PRIOR FILING DATE: 2000-10-18
 14 <150> PRIOR APPLICATION NUMBER: US 60/160,285
 15 <151> PRIOR FILING DATE: 1999-10-19
 16 <150> PRIOR APPLICATION NUMBER: US 60/183,583
 17 <151> PRIOR FILING DATE: 2000-02-18
 18 <160> NUMBER OF SEQ ID NOS: 7
 19 <170> SOFTWARE: FastSEQ for Windows Version 4.0
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 22 <211> LENGTH: 1464
 23 <212> TYPE: DNA
 24 <213> ORGANISM: homo sapiens
 25 <400> SEQUENCE: 1

26	atgacatcta	agaattatcc	cgggacctac	cccaatcaca	ctgtttgcga	aaagacaatt	60
27	acagtaccaa	aggggaaaag	actgattctg	aggttgggag	atttggatat	cgaatcccag	120
28	acctgtgctt	ctgactatct	tctcttcacc	agctcttcag	atcaatatgg	tccatactgt	180
29	ggaagtatga	ctgttcccaa	agaactcttg	ttgaacacaa	gtgaagtaac	cgtccgcttt	240
30	gagagtggat	cccacatttc	tggccggggg	tttttgctga	cctatgcgag	cagcgaccat	300
31	ccagatttaa	taacatgttt	ggaacgagct	agccattatt	tgaagacaga	atacagcaaa	360
32	ttctgcccag	ctggttgtag	agacgtagca	ggagacattt	ctgggaatat	ggtagatgga	420
33	tatagagata	cctctttatt	gtgcaaagct	gccatccatg	caggaataat	tgctgatgaa	480
34	ctaggtggcc	agatcagtg	gcttcagcgc	aaagggatca	gtcgatatga	agggattctg	540
35	gccaatggtg	ttctttcgag	ggatgggtcc	ctgtcagaca	agcgatttct	gtttacctcc	600
36	aatggttgca	gcagatcctt	gagttttgaa	cctgacgggc	aaatcagagc	ttcttcctca	660
37	tggcagtcgg	tcaatgagag	tggagaccaa	gttcactggg	ctcctggcca	agcccgaactt	720
38	caggaccaag	gcccacatg	ggcttcgggc	gacagtagca	acaaccacaa	accacgagag	780
39	tggctggaga	tcgatttggg	ggagaaaaag	aaaataacag	gaattaggac	cacaggatct	840
40	acacagtcca	acttcaactt	ttatgttaag	agttttgtga	tgaacttcaa	aaacaataat	900
41	tetaagtgga	agacctataa	aggaattgtg	aataatgaag	aaaaggtggt	tcagggtaac	960
42	tetaactttc	gggacccagt	gcaaaacaat	ttcatccctc	ccatcgtggc	cagatatgtg	1020
43	cgggttgtec	cccagacatg	gcaccagagg	atagccttga	agggtggagct	cattggttgc	1080
44	cagattacac	aaggtaatga	ttcattgggtg	tggcgcaaga	caagtcaaag	caccagtgtt	1140

ENTERED

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45      tcaactaaga aagaagatga gacaatcaca aggcccatcc cctcggaaga aacatccaca      1200
46      ggaataaaca ttacaacggt ggctattcca ttggtgctcc ttgttgctct ggtgtttgct      1260
47      ggaatgggga tctttgcagc ctttagaaag aagaagaaga aaggaagtcc gtatggatca      1320
48      gcgagggtc agaaaacaga ctgttggaag cagattaaat atccctttgc cagacatcag      1380
49      tcagctgagt ttaccatcag ctatgataat gagaaggaga tgacacaaaa gttagatctc      1440
50      atcacaagtg atatggcagg ttaa                                     1464
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53 <211> LENGTH: 487
54 <212> TYPE: PRT
55 <213> ORGANISM: homo sapiens
56 <400> SEQUENCE: 2
57      Met Thr Ser Lys Asn Tyr Pro Gly Thr Tyr Pro Asn His Thr Val Cys
58      1          5          10          15
59      Glu Lys Thr Ile Thr Val Pro Lys Gly Lys Arg Leu Ile Leu Arg Leu
60      20          25          30
61      Gly Asp Leu Asp Ile Glu Ser Gln Thr Cys Ala Ser Asp Tyr Leu Leu
62      35          40          45
63      Phe Thr Ser Ser Ser Asp Gln Tyr Gly Pro Tyr Cys Gly Ser Met Thr
64      50          55          60
65      Val Pro Lys Glu Leu Leu Leu Asn Thr Ser Glu Val Thr Val Arg Phe
66      65          70          75          80
67      Glu Ser Gly Ser His Ile Ser Gly Arg Gly Phe Leu Leu Thr Tyr Ala
68      85          90          95
69      Ser Ser Asp His Pro Asp Leu Ile Thr Cys Leu Glu Arg Ala Ser His
70      100         105         110
71      Tyr Leu Lys Thr Glu Tyr Ser Lys Phe Cys Pro Ala Gly Cys Arg Asp
72      115         120         125
73      Val Ala Gly Asp Ile Ser Gly Asn Met Val Asp Gly Tyr Arg Asp Thr
74      130         135         140
75      Ser Leu Leu Cys Lys Ala Ala Ile His Ala Gly Ile Ile Ala Asp Glu
76      145         150         155         160
77      Leu Gly Gly Gln Ile Ser Val Leu Gln Arg Lys Gly Ile Ser Arg Tyr
78      165         170         175
79      Glu Gly Ile Leu Ala Asn Gly Val Leu Ser Arg Asp Gly Ser Leu Ser
80      180         185         190
81      Asp Lys Arg Phe Leu Phe Thr Ser Asn Gly Cys Ser Arg Ser Leu Ser
82      195         200         205
83      Phe Glu Pro Asp Gly Gln Ile Arg Ala Ser Ser Ser Trp Gln Ser Val
84      210         215         220
85      Asn Glu Ser Gly Asp Gln Val His Trp Ser Pro Gly Gln Ala Arg Leu
86      225         230         235         240
87      Gln Asp Gln Gly Pro Ser Trp Ala Ser Gly Asp Ser Ser Asn Asn His
88      245         250         255
89      Lys Pro Arg Glu Trp Leu Glu Ile Asp Leu Gly Glu Lys Lys Lys Ile
90      260         265         270
91      Thr Gly Ile Arg Thr Thr Gly Ser Thr Gln Ser Asn Phe Asn Phe Tyr
92      275         280         285
93      Val Lys Ser Phe Val Met Asn Phe Lys Asn Asn Asn Ser Lys Trp Lys
94      290         295         300

```

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95      Thr Tyr Lys Gly Ile Val Asn Asn Glu Glu Lys Val Phe Gln Gly Asn
96      305                      310                      315                      320
97      Ser Asn Phe Arg Asp Pro Val Gln Asn Asn Phe Ile Pro Pro Ile Val
98                      325                      330                      335
99      Ala Arg Tyr Val Arg Val Val Pro Gln Thr Trp His Gln Arg Ile Ala
100                      340                      345                      350
101      Leu Lys Val Glu Leu Ile Gly Cys Gln Ile Thr Gln Gly Asn Asp Ser
102                      355                      360                      365
103      Leu Val Trp Arg Lys Thr Ser Gln Ser Thr Ser Val Ser Thr Lys Lys
104                      370                      375                      380
105      Glu Asp Glu Thr Ile Thr Arg Pro Ile Pro Ser Glu Glu Thr Ser Thr
106      385                      390                      395                      400
107      Gly Ile Asn Ile Thr Thr Val Ala Ile Pro Leu Val Leu Leu Val Val
108                      405                      410                      415
109      Leu Val Phe Ala Gly Met Gly Ile Phe Ala Ala Phe Arg Lys Lys Lys
110                      420                      425                      430
111      Lys Lys Gly Ser Pro Tyr Gly Ser Ala Glu Ala Gln Lys Thr Asp Cys
112                      435                      440                      445
113      Trp Lys Gln Ile Lys Tyr Pro Phe Ala Arg His Gln Ser Ala Glu Phe
114      450                      455                      460
115      Thr Ile Ser Tyr Asp Asn Glu Lys Glu Met Thr Gln Lys Leu Asp Leu
116      465                      470                      475                      480
117      Ile Thr Ser Asp Met Ala Gly
118                      485

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120 <210> SEQ ID NO: 3

121 <211> LENGTH: 1761

122 <212> TYPE: DNA

123 <213> ORGANISM: homo sapiens

124 <400> SEQUENCE: 3

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125      atgggattcg gtgcggggca gcgactgcgc cccgtcccgg cgccgcgctc gtccgcagag      60
126      gaggcggccc ggcccgggca gctgcggctc gggatccgtc gaggggaggc cgagcttgcc      120
127      aagctggcgc ccagcggggt catggtgccc ggcgcgccgc gcggcggcgc actggcgcg      180
128      gctgccgggc ggggcctcct ggctttgctg ctgcgcgtct ccgcccgcgt ccggctgcag      240
129      gcggaggagc tgggtgatgg ctgtggacac ctagtgactt atcaggatag tggcacaatg      300
130      acatctaaga attatcccgg gacctacccc aatcacactg tttgcgaaaa gacaattaca      360
131      gtaccaaagg ggaaaagact gattctgagg ttgggagatt tggatatcga atcccagacc      420
132      tgtgcttctg actatcttct cttcaccagc tcttcagatc aatatggtcc atactgtgga      480
133      agtatgactg ttcccaaaga actcttgttg aacacaagtg aagtaaccgt ccgctttgag      540
134      agtggatccc acatttctgg ccgggggttt ttgctgacct atgcgagcag cgaccatcca      600
135      gatttaataa catgtttgga acgagctagc cattatttga agacagaata cagcaaattc      660
136      tgcccagctg gttgtagaga cgtagcagga gacatttctg ggaatatggt agatggatat      720
137      agagatacct ctttattgtg caaagctgcc atccatgcag gaataattgc tgatgaacta      780
138      ggtggccaga tcagtgtgct tcagcgcaaa gggatcagtc gatatgaagg gattctggcc      840
139      aatggtgttc tttcgaggga tggttccctg tcagacaagc gatttctgtt tacctccaat      900
140      ggttgcagca gaccttgag ttttgaacct gacgggcaaa tcagagcttc ttcctcatgg      960
141      cagtcggtca atgagagtgg agaccaagtt cactgggtctc ctggccaagc ccgacttcag      1020
142      gaccaaggcc catcatgggc ttccggcgac agtagcaaca accacaaacc acgagagtgg      1080
143      ctggagatcg atttggggga gaaaaagaaa ataacaggaa ttaggaccac aggatctaca      1140
144      cagtcgaact tcaactttta tgtaagagt tttgtgatga acttcaaaaa caataattct      1200

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145 aagtggaaga cctataaagg aattgtgaat aatgaagaaa aggtgtttca gggtaactct 1260
146 aactttcggg acccagtgcg aaacaatttc atccctccca tegtggccag atatgtgcgg 1320
147 gttgtccccc agacatggca ccagaggata gccttgaagg tggagctcat tggttgccag 1380
148 attacacaag gtaatgattc attggtgtgg cgcaagacaa gtcaaagcac cagtgtttca 1440
149 actaagaaag aagatgagac aatcacaaag cccatcccct cggaagaaac atccacagga 1500
150 ataaacatta caacggtggc tattccattg gtgctccttg ttgtcctggt gtttgcctga 1560
151 atggggatct ttgcagcctt tagaaagaag aagaagaaag gaagtcctga tggatcagcg 1620
152 gaggctcaga aaacagactg ttggaagcag attaaatatc cctttgccag acatcagtca 1680
153 gctgagttta ccatcagcta tgataatgag aaggagatga cacaaaagtt agatctcatc 1740
154 acaagtgata tggcaggtta a 1761
156 <210> SEQ ID NO: 4
157 <211> LENGTH: 586
158 <212> TYPE: PRT
159 <213> ORGANISM: homo sapiens
160 <400> SEQUENCE: 4
161 Met Gly Phe Gly Ala Gly Gln Arg Leu Arg Pro Val Pro Ala Pro Arg
162 1 5 10 15
163 Ser Ser Ala Glu Glu Ala Ala Arg Pro Gly Gln Leu Arg Leu Gly Ile
164 20 25 30
165 Arg Arg Gly Glu Ala Glu Leu Ala Lys Leu Ala Pro Ser Gly Val Met
166 35 40 45
167 Val Pro Gly Ala Arg Gly Gly Gly Ala Leu Ala Arg Ala Ala Gly Arg
168 50 55 60
169 Gly Leu Leu Ala Leu Leu Leu Ala Val Ser Ala Pro Leu Arg Leu Gln
170 65 70 75 80
171 Ala Glu Glu Leu Gly Asp Gly Cys Gly His Leu Val Thr Tyr Gln Asp
172 85 90 95
173 Ser Gly Thr Met Thr Ser Lys Asn Tyr Pro Gly Thr Tyr Pro Asn His
174 100 105 110
175 Thr Val Cys Glu Lys Thr Ile Thr Val Pro Lys Gly Lys Arg Leu Ile
176 115 120 125
177 Leu Arg Leu Gly Asp Leu Asp Ile Glu Ser Gln Thr Cys Ala Ser Asp
178 130 135 140
179 Tyr Leu Leu Phe Thr Ser Ser Ser Asp Gln Tyr Gly Pro Tyr Cys Gly
180 145 150 155 160
181 Ser Met Thr Val Pro Lys Glu Leu Leu Leu Asn Thr Ser Glu Val Thr
182 165 170 175
183 Val Arg Phe Glu Ser Gly Ser His Ile Ser Gly Arg Gly Phe Leu Leu
184 180 185 190
185 Thr Tyr Ala Ser Ser Asp His Pro Asp Leu Ile Thr Cys Leu Glu Arg
186 195 200 205
187 Ala Ser His Tyr Leu Lys Thr Glu Tyr Ser Lys Phe Cys Pro Ala Gly
188 210 215 220
189 Cys Arg Asp Val Ala Gly Asp Ile Ser Gly Asn Met Val Asp Gly Tyr
190 225 230 235 240
191 Arg Asp Thr Ser Leu Leu Cys Lys Ala Ala Ile His Ala Gly Ile Ile
192 245 250 255
193 Ala Asp Glu Leu Gly Gly Gln Ile Ser Val Leu Gln Arg Lys Gly Ile
194 260 265 270

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195   Ser Arg Tyr Glu Gly Ile Leu Ala Asn Gly Val Leu Ser Arg Asp Gly
196           275                     280                     285
197   Ser Leu Ser Asp Lys Arg Phe Leu Phe Thr Ser Asn Gly Cys Ser Arg
198           290                     295                     300
199   Ser Leu Ser Phe Glu Pro Asp Gly Gln Ile Arg Ala Ser Ser Ser Trp
200           305                     310                     315                     320
201   Gln Ser Val Asn Glu Ser Gly Asp Gln Val His Trp Ser Pro Gly Gln
202           325                     330                     335
203   Ala Arg Leu Gln Asp Gln Gly Pro Ser Trp Ala Ser Gly Asp Ser Ser
204           340                     345                     350
205   Asn Asn His Lys Pro Arg Glu Trp Leu Glu Ile Asp Leu Gly Glu Lys
206           355                     360                     365
207   Lys Lys Ile Thr Gly Ile Arg Thr Thr Gly Ser Thr Gln Ser Asn Phe
208           370                     375                     380
209   Asn Phe Tyr Val Lys Ser Phe Val Met Asn Phe Lys Asn Asn Asn Ser
210           385                     390                     395                     400
211   Lys Trp Lys Thr Tyr Lys Gly Ile Val Asn Asn Glu Glu Lys Val Phe
212           405                     410                     415
213   Gln Gly Asn Ser Asn Phe Arg Asp Pro Val Gln Asn Asn Phe Ile Pro
214           420                     425                     430
215   Pro Ile Val Ala Arg Tyr Val Arg Val Val Pro Gln Thr Trp His Gln
216           435                     440                     445
217   Arg Ile Ala Leu Lys Val Glu Leu Ile Gly Cys Gln Ile Thr Gln Gly
218           450                     455                     460
219   Asn Asp Ser Leu Val Trp Arg Lys Thr Ser Gln Ser Thr Ser Val Ser
220           465                     470                     475                     480
221   Thr Lys Lys Glu Asp Glu Thr Ile Thr Arg Pro Ile Pro Ser Glu Glu
222           485                     490                     495
223   Thr Ser Thr Gly Ile Asn Ile Thr Thr Val Ala Ile Pro Leu Val Leu
224           500                     505                     510
225   Leu Val Val Leu Val Phe Ala Gly Met Gly Ile Phe Ala Ala Phe Arg
226           515                     520                     525
227   Lys Lys Lys Lys Lys Gly Ser Pro Tyr Gly Ser Ala Glu Ala Gln Lys
228           530                     535                     540
229   Thr Asp Cys Trp Lys Gln Ile Lys Tyr Pro Phe Ala Arg His Gln Ser
230           545                     550                     555                     560
231   Ala Glu Phe Thr Ile Ser Tyr Asp Asn Glu Lys Glu Met Thr Gln Lys
232           565                     570                     575
233   Leu Asp Leu Ile Thr Ser Asp Met Ala Gly
234           580                     585

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236 <210> SEQ ID NO: 5

237 <211> LENGTH: 1620

238 <212> TYPE: DNA

239 <213> ORGANISM: homo sapiens

240 <400> SEQUENCE: 5

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242   gctttgctgc tcgcggtctc cgccccgctc cggtctgcagg cggaggagct gggtgatggc      120
243   tgtggacacc tagtgactta tcaggatagt ggcacaatga catctaagaa ttatcccggg      180
244   acctacccca atcacactgt ttgcgaaaag acaattacag taccaaaggg gaaaagactg      240

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VERIFICATION SUMMARY

PATENT APPLICATION: US/10/813,588

DATE: 09/02/2004

TIME: 07:43:29

Input Set : N:\Crf3\RULE60\10813588.raw.txt

Output Set: N:\CRF4\09022004\J813588.raw

L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date